Sequence Alignment between see and sege ? SEQ ID NO: 11 of 10/051,835 and sege ? SEQ ID NO: 7 of 09/996952 (or U.S Pub. NO. SEQ ID NO: 7 of 09/996952 (or U.S Pub. NO. 2003/0170627)

	NUMBER OF SPO ID NOS: 194 SOFTWARE: PERL Program SEQ ID NO 226 LENGTH: 509	; FILE REFERENCE: PX-0037 P ; CURRENT APPLICATION NUMBER: US/09/974,298 ; CURRENT FILING MATE: 2001-10-04 ; PRIOR APPLICATION NUMBER: 60/238,331 ; PRIOR FILING MATE: 2000-05-10	-Mei	RESULT 1 US-09-974-298-126 Sequence 126. Application US/09974298	ALIGNMENTS	3 360.4 70.8 362 4 360.4 70.8 362 5 359.8 70.7 427	382.6 75.2 645 36 361.8 71.1 426 34 361.8 71.1 426 75	382.6 75.2 645 16 382.6 75.2 645 18	412.6 81.1 484 3.4 412.6 81.1 484 7. 202.6 81.1 484 7.	452.8 89.0 513 7: 435.2 85.5 563 2:	480.6 94.4 532 48 457.8 89.9 550 44 556 89.6 494	480.6 94.4 532 20 480.6 94.4 532 20 480.6 94.4 532 48	483.4 95.0 659 49 483.4 95.0 659 49 483.4 95.0 659 49 483.4 95.0 659 49	98.0 547 95.0 659 1 95.0 659	504.6 99.1 517 34 504.6 99.1 517 74 504.2 99.1 520 1 499 98.0 547 1	09 100.0 509 84 .8 99.4 871 1 .8 99.4 871 54	509 100.0 509 73 US-60-172-37 509 100.0 509 80 US-60-238-33 509 100.0 509 82 US-60-253-42	509 100.0 509 43 509 100.0 509 43 509 100.0 509 44	% Query re Match Length DB ID
D CV	Quer Best Mato	VS-09-		CUR CUR NUM SOP SEO		Sequence 7947, Ap ; Sequence 7947, Ap ; C Sequence 4606, Ap ;	13741, A RESULT 2 13 Sequence 30733, A RESULT 2 13 Sequence 30733, A US-09-996-		Sequence 6618, Ap Sequence 6618, Ap Sequence 6618, Ap	sequence sequence sequence	Sequence 4519, Ap Sequence 109, App Sequence 101, App	Sequence Sequence Sequence		Sequence Sequence Sequence Sequence	Sequence 1213 Sequence 1213 Sequence 38, F Sequence 3717,	Sequence Sequence 7 Sequence Sequence	Sequence 13437, A Sequence 126, App Sequence 7, Appli	Sequence 126, App Sest Los Sequence 7, Appli Matches Sequence 11, Appl Sequence 35, Appl Qy	on US-0
1 GAGTTGTGAGGGTGTGAGGGTCGCGTTCCTGCTGTCTGGACTTTTTCTGTCCCACTGAGA 60	Query Match 100.0%; Score 509; DB 42; Length 509; Best Local Similarity 100.0%; Pred. No. 2e-124; Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	: misc FORMATI 2-7	NGTH: 509 PE: DNA GANISM: Homo sapiens	CURRENT FILING DATE: 2001-11-27 CURRENT FILING DATE: 2001-11-27 NUMBER OF SEQ ID NOS: 9 SOFTWARE: PERL Program SEQ ID NO 7	LICANT: Wong, Sophia Mi-Ling LE OF INVENTION: CDNAS CO-EXPRESSED WITH PLACENTAL STEROID SYNTHESIS GENES E REFERENCE: PB-0016 US	equence 7, Application US/09996952 ENERAL INFORMATION: APPLICANT: Walker, Michael G.	ø	481 AACTTTTGCAGCTTTCTCCAAAAAAAA 509		ATCANAATA	361 APCAGAACAATTTAAAATGCCAGAAGGRAGGTGACAGGCAACAGGTTTAAATGAAGAC 420	301 GTCAAAGACTGGGGGTGAATGTGGAAATGGTCCTGATGACCAGGGGAAGATTCTGCCAAA 360 	241 TCAGGGTGCAGCTGAGACTZÁAGTGCCTGAACCTGGAAGCTGATCTCCAGGAGCTGTCTCA 300 	181 GCAAGAGGAACCACCAACTGAAAGTCGGGATCCTGCACCTGGTCAGGAGAGAAGAAGA 240				Local Similarity 100.0%; Pred. No. 2e-124; hes 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 GAGTTGTGAGGGTGTGAGGGTCGGGTTCCTGCTGTGTGTG	INFORMATION: Incyte ID No: 064516CB1 -298-126

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481 AACTTTGCAGCTTTCTCCAAAAAAAA 509 	421 AAGCTGAAACACAAAACTGTTTTATCTAAGATATTTGACTTAAAAATATCGAAATA 480	361 APĆAGAACAATTTAAAATGCCAGAAGGAGGTGACAGGCAACCACAGGCTTTAAATGAAGAC 420	301 GTCAAAGACT9dGGGTGAATGTGGAAATGGTCCTGATGACCAGGGGAAGATTCTGCCAAA 360 	241 TCAGGGTGCAGCTGAGACTZAAGTGCCTGAACCTGAAGCTGATCTCCAGGAGCTGTCTCA 300 	181 GCAAGAGGAACCACCAACTGAAAGTCGAGATCCTGCACCTGGTCAGGAGAGAAGAAGAAGAAGA 240	121 AAGTGTACCACCTCCTGAGCTGATTGGGCCTATGCTGGAGGCCGGTGATGAGGAGGCCTCA 180	61 CGCAGCTGTGAAATATGATTTGGCGAGGAAGATCAACATATAGGCCTAGGCCGAGGAG 120 	1 GAGTIGIGAGGGIGIGAGGGICGCGITCCIGCTGICTGGACTTITTCIGICCCACZGAGA 60	Match 100.0%; Score 509; DB 41; Length 509; Local Similarity 100.0%; Pred. No. 2e-124; es 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	R INFORMATION: Incyte ID No: 064516CBI

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NAME/KEY: misc_feature
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Best Local Sim
Matches 509;
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ORDERAL INFORMATION:
ARPLICANT: JONES, David A.
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN TUMOR CELLS
FILE REFERENCE: PA-0044 US
CURRENT APPLICATION NUMBER: US/10/051,835
CURRENT FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PERIL PROGRAM
SEC ID NO 11
FEBORAL 5 CO.
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                                                                                                                                                                                                                                                                                                     LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte
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Sequence 35, Application US/10093766
GENERAL INFORMATION:
APPLICANT: Lissek, Amy W.
APPLICANT: Jones, David A.
APPLICANT: Karpt, Adam R.
APPLICANT: Karpt, Adam R.
APPLICANT: BAPT, ADAM R.
APPLICANT: BAPT, ADAM R.
APPLICANT: MAPPL, ADAM R.
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; FEATURE;
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
US-10-093-766-35
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CURRENT FILING DATE: 2002-03-0
NUMBER OF SEQ ID NOS: 61
SOPTWARE: PERL Program
SEQ ID NO 35
LENGTH: 509
TYPE: DNA
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US-10-093-766-35
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Best Local Similarity
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Pred. No. 2e-124;
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Sequence 126, Application US/09974298

GENERAL INFORMATION:
APPLICANT: Chen, Hust Mei
TITLE OF INVENTION GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: P\$-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298

CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SPO ID NOS: 194
SEC ID NO 426
SEC ID NO 426
LENGTH; 509

LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: misc_feature

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GAGTIGIGAGGGTGGAGGGTCCCGCTTCCTGGACTTTTTCTGTCCCACTGAGA

Query Match
Best Local Similarity
Matches 509; Conserv

Conservative

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100.0%;

Score 509; DB 42 Pred. No. 2e-124;); Mismatches 0

42; 0;

Indels Length

0

Gaps

60 60

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KBY: misc_feature
; OTHER INFORMATION: Incyte ID No: 253708
US-09-996-952-7

TYPE: DNA

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LENGTH: 509
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Best Local Similarity
Matches 509; Conserv
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APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES REGULATED BY DNA
FILE REFERENCE: PA-0044 US
CURRENT APPLICATION NUMBER: US/10/051,835
CURRENT FIXING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 25
SOFTMALE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-051-835-11
                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No:
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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GAGTTGTGAGGGTGTGAG
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llarity 100.0%; Pred. No.
Conservative 0; Mismatch
                                      FACCACCTCCTGAGCTGATTGGGCCTATGCTGGAGCCCGGTGATGAGGAGCCTCA 180
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GCAAGAACCACCAACTGAAAGTCGGGATCCTGCACCTGGTCAGGAGAGAAGAAGAAGA

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APPLICANT: LASEK, AMWW.
APPLICANT: Jones, David A.
APPLICANT: Marpf, Adam'R.
TITLE OF INVENTION: GENEX REGULA
FILE REFERENCE: PA-0047 UK
CURRENT APPLICATION NUMBER US/1
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL PROGram
SEQ ID NO 35
LENGTH: 509
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID NO
US-10-03-766-35
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                 301
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                                                                                                                                                                                                                                                                      121 AAGTGTACCACCTCCTGAGCTGATTGGGCCTATGCTGGAGCCCGG
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                                                                 GTCAAAGACTGGGGGTGAATGTGGAAAATGGTCCTGATGACCAGGGGGAAGATTCTGCC
                                                                                                   TCAGGGTGCAGCTGAGACTCAAGTGCCTGACCTGGAAGCTGATCTCCAGGAGCTG
                                                                                                                         TCAGGGTGCAGCTGAAGTGCCTGACCTGGAAGCTGATCTCCAGGAGG
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Pred. No. 2e-124;
Mismatches 0
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Sequence Alignment between and 500 =0 no:11 of 10/051,835 and 500 =0 no:35 of 10/093,766

page 1 of 2 Page 3

Db 361 ATCACARACTATARATACCARACACARACTATTTTACCTARACTATTTTCACCTARAATATA 480 27 41 AGCTCHARACAACACARACACARACACARACACACACACACACA

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GENERAL INFORMATION:
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Best Local (
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APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Liep, Dish
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms (U)
TITLE OF INVENTION: Polymucleotide Sequence Databases, and Single Nucleotide Interest Taylor of Sequence Databases, and Single Nucleotide Interest Taylor of Sequence Us/60/172,377
CURRENT APPLICATION NUMBER: US/60/172,377
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 13,749
SOFTWARE: PERL Program
SEQ ID NO 13437
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OTHER INFORMATION: In-
-60-172-377-13437
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equence 13437, Ap
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ORGANISM: Homo sap
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Pred. No. 2e-124;
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FEATURE:
NAME/KEY: MISC feature
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GENERAL INFORMATION:
       Requence 7, Application US/60253425
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Wong, Sophia Mi-Ling
TITLE OF INVENTION: CDNAS CO-EXPRESSED W:
FILE REFERENCE: BB-0016 P
FILE REFERENCE: BB-0016 P
CURRENT APPLICATION NUMBER: US/60/253,425
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Matches 509; Conser
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                                                          CDNAS CO-EXPRESSED WITH PLACENTAL STEROID SYNTHESIS GRNES
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100.0%; Pred. No. 2e-124;
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SES 10 no: 692

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RESULT 1

US-10-044-090-692
; Sequence 692, Application US/10044090
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 692
; LENGTH: 2484
; TYPE: DNA
; COLUMN SERVER SE ; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID.
US-10-044-090-692 Query Match Length 2484 26231 26231 757 1661 1678 1714 1714 1714 1529 1529 1811 2527 1892 1892 1892 1892 548 757 B 101 103 US-10-03-1-407-80
US-10-10-755-889-219
US-60-440-068-219
US-60-469-757-219
US-60-260-493-519
US-60-278-258-11926
US-09-644-867-6745
US-09-652-111-9321
US-09-652-111-9321
US-09-652-111-9321
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US-09-652-111-9321
US-09-652-111-9321
US-09-652-111-3321
US-09-652-111-3321
US-09-652-111-3324 US-10-044-090-692
US-10-051-835-18
US-60-262-451-18
US-60-262-451-18
US-60-262-451-193
US-60-466-412-85903
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US-60-466-412-85903
US-60-485-450-12087
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US-10-247-671-82
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US-60-323-784-86
US-60-323-784-86
US-60-359-922-657
US-99-359-922-657
US-99-359-922-657
US-99-844-868-8607
US-99-359-922-657
US-99-359-922-657
US-99-359-922-657
US-99-844-868-8607
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US-99-844-868-8607 No: f 60-50 08-09-08-10-50 08-09-ខ្លួច ALIGNMENTS 231486.18 IN VASCULAR TISSUE ACTIVATION Sequence 56, Appl sequence 82, Appl sequence 867, App sequence 657, App sequence 10028, App sequence 10028, App sequence 518, App sequence 519, App sequence 4809, App sequence 5180, App sequence 5180, App sequence 4809, App sequence 4809, App sequence 4809, App sequence 5180, App sequence 5180, App sequence 4809, App sequence 5180, App sequence 4809, App sequence 4809, App sequence 4809, App sequence 5180, App sequence 5 Description Sequence Sequence Sequence Sequence Sequence 11923, A Sequence 52325, A Sequence 85903, A Sequence 12087, A Appl 1923, A 문 8 5 Ş 문 닭 Ś 片 δ 유 Ś 맑 Ś B 5 밁 Ş 8 S 片 δ Ś 밁 뫄 S 밁 맑 δ S 밁 δ 유 Query Match Best Local (Matches 961 961 841 781 721 661 661 601 601 541 781 721 541 481 481 421 421 361 361 301 301 241 2484; 241 181 TCCCCTCTTCCCATTAGTAACCATATAAAATTTATATTTTACTTGCCTTTTTAAAATATGT 181 121 121 61 .u 100.0%; Score 2484; Similarity 100.0%; Pred. No. 0; 84; Conservative 0; Mismathhan CTCCTCTCAGATGATAGTAAAGATCAAAAGAATTCGAAGGGAGTTGGTAAACGCTGGTGT CTCCTCAGATGATAGTAAAGATCAAAAGAATTCGAAGGGAGTTGGTAAACGCTGGTGT GCTGAAGGACAGAATTCATTGTGTGGCATTTGTATTTGATGCCAGCTCTATTCAATACTT GCTGAAGGACAGAATTCATTGTGTGGCATTTGTATTTGATGCCAGCTCTATTCAATACTT ACAGTTTAATCCCATGGAATCAATCAAATTAAATCATCATGACTACATTGATTCCCCCATC GGTACATAGTTTGTGCTCATAAATATTTTTTGAATTAATATCTTGCTTTATGTCTACCTT CCTCATACTATTAGAGACTTTTCTGTTTTGTTTTACCATTTGATTCACTTTGCACAGAGTGCCT TAGGTGAAAGGACTGCTGGCTTACTTGCATAATGCCTGTCTTCTCTACCAAGATTGTTAG CACTCCTGCTATTTTAGCTCTCAGATTACATGTCCTTTCCTCACAGAGGCCTTACTTGAC GCAGATIGCCTCTTATCTAGAACACTTTCAGCCATATCCTTATTCTCTTTAGCAGACT GCAGTTAATAATCTTTGCATATATCATTTTGCATTTTTGTCAGTATATCAGTGGGACAGA TATATTGACTTATCAGACATTGTTTAACTGACATGGCATTTTTCTGCTACAAATGTTCCA TATATTGACTTATCAGACATTGTTTAACTGACATGGCCATTTTTCTGCTACAAATGTTCCA GGTACATAGTTTGTGCTCATAAATATTTTTTGAATTAATATCTTGCTTTATGTCTACCTT CCTCATACTATTAGAGACTTTTCTGTTTTGTTTACCATTTGATTCACTTGCACAGTGCCT TAGGTGAAAGGACTGCTGCCTTACTTGCATAATGCCTGTCTTCTCTACCAAGATTGTTAG CACTCCTGCTATTTTAGCTCTCAGATTACATGTCCTTTCCTCACAGAGGCCTTACTTGAC CTTGCGCTCTGCTTGATGGTACCAGCTTTTTTTTCTGAATGCTCTTACTTCCATCTGTGG AACAAAGTACATATAAATTTGCTGCTACTCCCTTCTTAGAGAAGTGGTAGAAAACTATGT TCCCCTCTTCCCATTAGTAACCATATAAAATTTATATTTTACTTGCCTTTTAAAAAATATGT TACAAAATAATGTATAGTCAAAGAATCTATCTTCCTTCTCTGCCCCTTCAAATAAAATTTC CTTGCGCTCTGCTTGATGGTACCAGCTTTTT TTCCCAACAGAGAAGTGCTAGATGAAGAGTAAAGTCATCTCACCTTGGACCCCTTCCCTC TTCCCAACAGAGAAGTGCTAGATGAAGAGTAAAGTCATCTCACCTTGGACCCCTTCCCTC GCAGTTAATAATCTTTGCATATATCATTTTTGCATTTTTGTCAGTATATCAGTGGGACAGA AACAAAGTACATATAAATTTGCTGCTACTCCCTTCTTAGAGAAGTGGTAGAAAACTATGT TGTTAAGITAATTIGGITTTATAITTATATGTTTAGCATTTATGTIGGTTCAAAGATCAAATC TGTTAAGTTAATTTGGTTTTATATTTATGTTTAGCATTTATGTGGTTTCAAAGATCAAATC GTTTATTCTTGTATTATAACCATAACAGTTCACTAATTAAATTTAAATTTAGGAATTGAAT GTTTATTCTTGTATTATAACCATAACAGTTCACTAATTAAATTAAATTTAGGAATTGAAT CTTATCTAGAACACTTTCAGCCATATCCTTATTCTCTTTAGCAGACT Mismatches TTTCTGAATGCTCTTACTTCCATCTGTGG DB 43; Length 2484; 0 Indels (or us pub. No 2002/0137081 ٥, 1020 960 900 900 840 840 780 720 660 660 600 540 540 420 720 480 480 420 360 780 360 300 300 240 180 180 120 120 60

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041 CATCCCTTC: 041 CATCCCTTC:
1 TTTAGTGO
801 TAATGCCA
741 TCATCTTAGI
621 GGACCTT 681 CCCCTT
501 GTTTT
1441 ATTITTCCCTCCTIGCATTTCCCTCTTTTCCTGA
321 GAAGCG 381 GTCTTT [
261 CTTCTT 261 CTTCTT 261 CTTCTT
141 TGGATT 201 CCCTGT
081 TATAGA 081 TATAGA
021 GGTACE 021 GGTACE

8 B 8

2221 AATAGATATTTCCCAAAGATCAAAGTTTCCCCACCACACAGAAAATTAAAATTCAGAAA Qy 2221 AATAGATAGATACTCAAAGATCACATAAATTCCCCACCACACAGAAAATTAAAATTCAGAA Db 2221 AATAGATACTCAGAAAATTCACATAAATTCCCCACCACACAGAAAATTAAAATTCAGAA Qy 2231 AGGAAAAAAAATCCCAAAAAATTCACATACCATACACAGAAAATTAAAATTCAGAAA Qy 2231 AGGAAAAAAAATCCAAAAAATTCAAAAATTCCACAAAAAAATTCCACAAATTAAATTCCAGAAATTAAATTCCAGAAATTCAAAATTCAGAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAATTCAAAAAA	2101
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1261 AAGATGGTKTTAGAAAAGCTTTGTCTAAAAATTTTGGCCTAGGAATGGTAACTTCATTTTCA 1320

GAAAGCTTTGTCTAAAAATTTGGCCTAGGAATGGTAACTYCATTTTCA 1320 AGAAAAATAATAIGTGTGTTATGTTATGTTTAAGATATTATTAG 1380

1201 TCATCTCAGGATGAATCTTTTATGTCTTTTTATTGTATGGATATCTGAATTTACT

TATA 1260

1201 TCANCTCAGGATGAATCTTTTATGTCTTTTTATTGTAAGGATATCTGAATTTTACTTTATA 1260

TATGCACATGTCAGAAAAAGGCAAGACAAATGGCCTCTTGTACTGAATACTTCGGCAAAC 1080

081 Trafredererreatrireneaeagaeagaetrigaeteaanarrigragaeetreegia 1196

GAATGGATTACATGGTAGTGATGCACTGGTAGAAATGGTTTTTAGTTATTGACTCAGAAT 1/200

ORATGGATTACATGGTAGTGATGCACTGGTAGAAATGGTTTTTAGTTATTGACTCAGAAY

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1381 GTACTATCAATGAATGTAYTTAAATATTTTTCATATTCTGTGACAAGCATTTATA¶TTTG 1440

AATATTTTCATATTCTGTGAZAAGCATTTATAATTTG

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1441 CAACAAGTGGAGTCCATTTAGCCCA

1441 CAACAAGTGGAGTCCATTTAGCCCAGTGGGAAAGTCTTGGAACTCTCAGGTTACCCTTGAAG 1500

RTGGGAAAGTCTTGGAACTCAGGTTACCCTTGAAG

1500

1561

1501 GATATGCTGGCAGCCATCTCTTTGATCTG

GATATGCTGGCAGCCATCTCTTTGATC\GTGCTTAAACTGTAATTTATAGACCAGCTAAA 1560

1561

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ATGTCTTACATTGATAAAATTCTTAAAGAGCAAAAACTGCATTTTATTTCTGCACCACAT 1860 ATGTCTTACATTGATAAAATTCTTAAAGAGCAAAACTGCATTTTATTTCTGCATCCACAT 1860

TCATCTG/GGATTGCGTTGTTTCTTAGGGTTCCTAGCACTGATGCCTGCACAAGCATGTG

1980

1741 1741 1681 1681 1621 1621

GAGTGATCCTCAATATCCTAACTAACTGGTCCTCAACTCAAGCAGAGTTTCTTCACTCTG 1740

GGCATCGTGGGTTTGGTGATTGAAAACACAAAAAAAGAAGAGATCCAGCTGAAAAA 1680

CAGAGAGATCCAGCTGAAAAA 1680

GGCATCGTGGGTTTGGTCTAGTGATXGAAAACACAAGA

TCCCTAACTTGGATCTGGAATGCATTAGTTAMACCTTGTACCATTCCCAGAATTTCAGG 1620

CTTGTACCATTCCCAGAATTTCAGG 1620

GCACTGTGATCATGAAACY/AGTAGAGGGGATTGTGTGTGTATTTT

MIACAAATTTAATACA 1800

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Qy 301 TATTTCAAAAGATTTCTGAATTAATTTTTCCCTAGAATTTCTCCTTCATTCCAAAGTACA 360	Oy 241 AGTCATATCACACTGGGAGGCAATGCAATGTGGTTACCTGGTCCTAGGTTTGAACTGTCT 300	QY 181 AAAATTTAGACATCAAATTTTCCTACTAACTTACTTAGTAGTGCATACTTGGAAGCAC 240	Qy 121 TGCATGTTTAAGCTGTATAATTTGTTGGGTTGTGAGTGGTCTGACTTAAATGTGTATTAT 180	QY 61 GAGTACCTIGTTGIGACAGGGTATTATTACAGCATCTTGIGGGAAAACCTATTAGGCCTT 120	Qy 1 GCCAGAGGGGAAAAAAGAGTAATGCACAGGTATCTCTTTTGCAGTGGTGACTGTATTTT 60	Query Match 100.0%; Score 2346; DB 44; Length 2346; Best Local Similarity 100.0%; Pred. No. 0; Matches 2346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TTGTATTTATATGTATTWEACCTGTCAGCTTCTAGTTGCTTCAACCA/	OY 2101 IGCTATGAAGTAAGTGTGTTTTGTTTTCATCTTATGGAAACTCTTGATGCATGTGTTTTG 2160
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1321 GTIGCCAAGGGTAGAAAATAATATIGTGTGTGTTATGTTTAAGATATATTATTAG 1380	1 ACCITACITICANGANICANACAGATIGITCCCATGANGENTIGITCATAGGICALICANACAGATIGITCCCATGANGENTIGITCATAGGICALICANACAGATIGITCCCATGANGENTIGITCATAGGICATAGATAGATIGITCCATGANGENTIGITCATAGATAGATIGATICATAGATAGATIGATICATAGATAGATAGATAGATAGATAGATAGATAGATAGATA
US-10-116-802-474 ; Sequence 474 Application US/10116802 ; Sequence 474 Application US/10116802 ; GENERAL INFORMATION: ; APPLICANT: Amy Lasek ; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER ; FILE REFERENCE-PA-0045 US ; CURRENT APPLICATION NUMBER: US/10/116,802	Qy 1441 CARCHOTOGRACTCCHTTPACCCAGTGGGAAAGTCTTGGAACTCCGGTTACCCTTGAAG 150 1441 CARCHOTOGRACTCCATTTACCCAGTGGGAAAGTCTTGGAACTCAAGTTACAGTTACCCTTGAAAC 150 Qy 1501 GRATUGCTGGGACCCACTCTTGGATCTTACACTTTACTTTAC

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Score

Match Query

Length

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Description

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US-09-974-298-126 US-09-996-952-7 US-10-051-835-11 US-10-053-766-35 US-10-093-766-35 US-60-172-377-13437 US-60-238-331-126

US-60-253-425-7 US-60-262-451-11 US-60-277-380-35

SEØ ID NO: 126 05/974, 258

; OTHER INFORMATION: Incyte ID No: 064516CB1 US-09-974-298-126 Query Match and SEW ID NO: 11 100.0%; Score 509; DB 41; 100.0%; Pred. No. 2e-124; Length 509;

Jeque...
Jequence 5280, Ap
Sequence 6618, Ap
Sequence 6619, Ap
Sequence 6290, Ap
Sequence 13741, A US-09-96-952-7
US-09-96-952-7
Sequence 7, Application US/09996952
SENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Wong, Sophia M.-Ling
ITILE OF ANCENTION: CDNAS CO-EXPRESSED WITH PLA
ITILE OF ANCENTON: CDNAS CO-EXPRESSED WITH PLA
ITILE OF ANCENTON NUMBER: US/09/996,952
CURRENT FILING DATS: 2001-11-27
NUMBER OF SEQ ID NOS: 4 ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; CTHER INFORMATION: Incyt
US-09-996-952-7 SOFTWARE: PERL Program EQ ID NO 7 ENGTH: 509 Incyte 253708 PLACENTAL STEROID SYNTHESIS GENES

ALIGNMENTS

452.8 452.8 452.1

483 480 480 480 480 480 480 480

Sequence 7668, App Sequence 12130, A Sequence 12130, A Sequence 38, Appl Sequence 3717, Ap Sequence 3717, Ap Sequence 3717, App Sequence 634, App Sequence 634, App Sequence 634, App Sequence 644, App Sequence 441, App Sequence 441, App Sequence 4519, Ap Sequence 109, App Sequence 109, App Sequence 6619, Ap Sequence 6619, Ap

421.4 412.6 412.6 393.8

PCT-US01-08631-5288 US-09-834-366-6618 US-60-197-873-6618 PCT-US01-08631-5290

US-10-072-012-111 US-09-834-366-6619 US-60-197-873-6619 US-09-652-918-5956

US-09-205-070-13741 US-09-340-623-13741

360 360 359

US-09-898-888-13741
US-09-898-888A-13741
US-09-894-888A-13741
US-09-834-366-30733
US-60-197-873-30733
US-09-489-036-7947
US-09-943-143-7947
US-09-943-143-7947
US-10-170-235-4606

Sequence Sequence Sequence Sequence 483.4

PCT US03-JB193-7668
4 US-10-723-860-7668
4 US-90-834-366-72130
5 US-60-197-873-12130
PCT-US02-09808-38

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NESULT 1
US-09-974-298-126
IS-09-974-298-126
Sequence 126, Application US/09974298
GENERAL INFORMATION: APPLICANT: Chen, Huei-Mei TITLE OF INVENTION: GENES EXPRESSED IN BREAST FILE REFERENCE: PA-0037 P CANCER

CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 126
LENGTH: 509

Pap TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

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Query Match 100.0%; Best Local Similarity 100.0%; Matches 509; Conservative 0

<u>,</u>

Score 509; DB 42 Pred. No. 2e-124; Mismatches

DB 42;

Indels Leagth 509;

0;

Gaps CTGAGA 60 0

GAGTTGTGAGGGTGTGAGGGTCGCGGTTCCTGCTGTCTGGACTTTTTCTGTCC